RAW SEQUENCE LISTING   DATE: 11/27/2001
PATENT APPLICATION: US/09/883,797   TIME: 12:54:48

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Output Set: N:\CRF3\11272001\I883797.raw

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 1 <110> APPLICANT: Jaworski, Jan G.
 2        Post-Beittenmiller, Martha A.
 3        Todd, James
 4 <120> TITLE OF INVENTION: FATTY ACID ELONGASES
 5 <130> FILE REFERENCE: 07148/06400î1
 6 <140> CURRENT APPLICATION NUMBER: 09/883,797
 7 <141> CURRENT FILING DATE: 2001-06-18
 8 <150> PRIOR APPLICATION NUMBER: 08/868,373
 9 <151> PRIOR FILING DATE: 1997-06-03
10 <160> NUMBER OF SEQ ID NOS: 22
11 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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15 <212> TYPE: DNA
16 <213> ORGANISM: Arabidopsis thaliana
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20       ggacttcaca actcttgcaa cgtgaccacc attctcttct tcttaattat tcttcctta    180
21       accggaaccg tgctggttca gctaaccggt ctaacgttcg atacgttctc tgagctttgg    240
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23       ttcgtttta ccctctacgt ggctaaccgg tctaaaccgg tttacctagt ggatttctcc    360
24       tgctacaaac cggaagacga gcgtaaaata tcagtagatt cgttcttgac gatgactgag    420
25       gaaaatggat cattcaccga tgacacggtt cagttccagc aaagaatctc gaaccgggcc    480
26       ggtttgggag acgagacgta tctgccacgt ggcataactt caacgccccc gaagctaaat    540
27       atgtcagagg cacgtgccga agctgaagcc gttatgtttg gagccttaga ttccctcttc    600
28       gagaaaccg gaattaaacc ggccgaagtc ggaatcttga tagtaaactg cagcttattc    660
29       aatccgacgc cgtctctatc agcgatgatc gtgaaccatt acaagatgag agaagacatc    720
30       aaaagttaca acctcggagg aatgggttgc tccgccggat taatctcaat cgatctcgct    780
31       aacaatctcc tcaaagcaaa ccctaattct tacgctgtcg tggtaagcac ggaaaacata    840
32       accctaaact ggtacttcgg aaatgaccgg tcaatgctcc tctgcaactg catcttccga    900
33       atgggcggag ctgcgattct cctctctaac cgccgtcaag accggaagaa gtcaaagtac    960
34       tcgctggtca acgtcgttcg aacacataaa ggatcagacg acaagaacta caattgcgtg   1020
35       taccagaagg aagacgagag aggaacaatc ggtgtctctt tagctagaga gctcatgtct   1080
36       gtcgccggag acgctctgaa aacaaacatc acgactttag gaccgatggt tcttccattg   1140
37       tcagagcagt tgatgttctt gatttccttg gtcaaaagga agatgttcaa gttaaaagtt   1200
38       aaaccgtata ttccggattt caagctagct ttcgagcatt tctgtattca cgcaggaggt   1260
39       agagcggttc tagacgaagt gcagaagaat cttgatctca aagattggca catggaacct   1320
40       tctagaatga ctttgcacag atttggtaac acttcgagta gctcgctttg gtatgagatg   1380
41       gcttataccg aagctaaggg tcgggttaaa gctggtgacc gactttggca gattgcgttt   1440
42       ggatcgggtt tcaagtgtaa tagtgcggtt tggaaagcgt tacgaccggt ttcgacggag   1500
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48 <213> ORGANISM: Arabidopsis thaliana
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53              20              25                      30
54      Val Lys Leu Lys Tyr Val Lys Leu Gly Leu His Asn Ser Cys Asn Val
55          35              40                      45
56      Thr Thr Ile Leu Phe Phe Leu Ile Ile Leu Pro Leu Thr Gly Thr Val
57          50              55                      60
58      Leu Val Gln Leu Thr Gly Leu Thr Phe Asp Thr Phe Ser Glu Leu Trp
59      65              70                      75                      80
60      Ser Asn Gln Ala Val Gln Leu Asp Thr Ala Thr Arg Leu Thr Cys Leu
61                      85                      90                      95
62      Val Phe Leu Ser Phe Val Leu Thr Leu Tyr Val Ala Asn Arg Ser Lys
63                  100                     105                     110
64      Pro Val Tyr Leu Val Asp Phe Ser Cys Tyr Lys Pro Glu Asp Glu Arg
65              115                     120                     125
66      Lys Ile Ser Val Asp Ser Phe Leu Thr Met Thr Glu Glu Asn Gly Ser
67          130                     135                     140
68      Phe Thr Asp Asp Thr Val Gln Phe Gln Gln Arg Ile Ser Asn Arg Ala
69      145                     150                     155                     160
70      Gly Leu Gly Asp Glu Thr Tyr Leu Pro Arg Gly Ile Thr Ser Thr Pro
71                  165                     170                     175
72      Pro Lys Leu Asn Met Ser Glu Ala Arg Ala Glu Ala Glu Ala Val Met
73                  180                     185                     190
74      Phe Gly Ala Leu Asp Ser Leu Phe Glu Lys Thr Gly Ile Lys Pro Ala
75              195                     200                     205
76      Glu Val Gly Ile Leu Ile Val Asn Cys Ser Leu Phe Asn Pro Thr Pro
77          210                     215                     220
78      Ser Leu Ser Ala Met Ile Val Asn His Tyr Lys Met Arg Glu Asp Ile
79      225                     230                     235                     240
80      Lys Ser Tyr Asn Leu Gly Gly Met Gly Cys Ser Ala Gly Leu Ile Ser
81                  245                     250                     255
82      Ile Asp Leu Ala Asn Asn Leu Leu Lys Ala Asn Pro Asn Ser Tyr Ala
83                  260                     265                     270
84      Val Val Val Ser Thr Glu Asn Ile Thr Leu Asn Trp Tyr Phe Gly Asn
85              275                     280                     285
86      Asp Arg Ser Met Leu Leu Cys Asn Cys Ile Phe Arg Met Gly Gly Ala
87          290                     295                     300
88      Ala Ile Leu Leu Ser Asn Arg Arg Gln Asp Arg Lys Lys Ser Lys Tyr
89      305                     310                     315                     320
90      Ser Leu Val Asn Val Val Arg Thr His Lys Gly Ser Asp Asp Lys Asn
91                  325                     330                     335
92      Tyr Asn Cys Val Tyr Gln Lys Glu Asp Glu Arg Gly Thr Ile Gly Val
93              340                     345                     350
94      Ser Leu Ala Arg Glu Leu Met Ser Val Ala Gly Asp Ala Leu Lys Thr
95          355                     360                     365
96      Asn Ile Thr Thr Leu Gly Pro Met Val Leu Pro Leu Ser Glu Gln Leu
97          370                     375                     380
98      Met Phe Leu Ile Ser Leu Val Lys Arg Lys Met Phe Lys Leu Lys Val
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101                      405                    410                    415
102      His Ala Gly Gly Arg Ala Val Leu Asp Glu Val Gln Lys Asn Leu Asp
103                      420                    425                    430
104      Leu Lys Asp Trp His Met Glu Pro Ser Arg Met Thr Leu His Arg Phe
105                435                    440                    445
106      Gly Asn Thr Ser Ser Ser Ser Leu Trp Tyr Glu Met Ala Tyr Thr Glu
107                450                    455                    460
108      Ala Lys Gly Arg Val Lys Ala Gly Asp Arg Leu Trp Gln Ile Ala Phe
109      465                    470                    475                    480
110      Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp Lys Ala Leu Arg Pro
111                      485                    490                    495
112      Val Ser Thr Glu Glu Met Thr Gly Asn Ala Trp Ala Gly Ser Ile Asp
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121 <400> SEQUENCE: 3
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124      caagatctcc aaaacttta cctctactta caaaacaacc acacatctct aaccatgttc        180
125      ttcctttacc tcgctctcgg gtcgactctt tacctcatga cccggcccaa acccgtttat       240
126      ctcgttgact ttagctgcta cctcccaccg tcgcatctca aagccagcac ccagaggatc       300
127      atgcaacacg taaggcttgt acgagaagca ggcgcgtgga agcaagagtc cgattacttg       360
128      atggacttct gcgagaagat tctagaacgt tccggtctag gccaagagac gtacgtaccc       420
129      gaaggtcttc aaactttgcc actacaacag aatttggctg tatcacgtat agagacggag       480
130      gaagttatta ttggtgcggt cgataatctg tttcgcaaca cgggaataag ccctagtgat       540
131      ataggtatat tggtggtgaa ttcaagcact tttaatccaa caccttcgct atcaagtatc       600
132      ttagtgaata agtttaaact tagggataat ataaagagct tgaatcttgg tgggatgggg       660
133      tgtagcgctg gagtcatcgc tatcgatgcg gctaagagct tgttacaagt tcatagaaac       720
134      acttatgctc ttgtggtgag cacggagaac atcactcaaa acttgtacat gggtaacaac       780
135      aaatcaatgt tggttacaaa ctgtttgttc cgtataggtg gggccgcgat tttgctttct       840
136      aaccggtcta tagatcgtaa acgcgcaaaa tacgagcttg ttcacaccgt gcgggtccat       900
137      accggagcag atgaccgatc ctatgaatgt gcaactcaag aagaggatga agatggcata       960
138      gttggggttt ccttgtcaaa gaatctacca atggtagctg caagaaccct aaagatcaat      1020
139      atcgcaactt tgggtccgct tgttcttccc ataagcgaga agtttcactt ctttgtgagg      1080
140      ttcgttaaaa agaagtttct caaccccaag ctaaagcatt acattccgga tttcaagctc      1140
141      gcattcgagc atttctgtat ccatgcgggt ggtagagcgc taattgatga gatggagaag      1200
142      aatcttcatc taactccact agacgttgag gcttcaagaa tgacattaca caggtttggt      1260
143      aatacctctt cgagctccat ttggtacgag ttggcttaca cagaagccaa aggaaggatg      1320
144      acgaaaggag ataggatttg gcagattgcg ttggggtcag gtttaagtg taatagttca      1380
145      gtttgggtgg ctcttcgtaa cgtcaagcct tctactaata atccttggga acagtgtcta      1440
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148 <210> SEQ ID NO: 4
149 <211> LENGTH: 493
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156                 20                  25                  30
157     Val Glu Ala Ser Arg Leu Ser Thr Gln Asp Leu Gln Asn Phe Tyr Leu
158             35                  40                  45
159     Tyr Leu Gln Asn Asn His Thr Ser Leu Thr Met Phe Phe Leu Tyr Leu
160         50                  55                  60
161     Ala Leu Gly Ser Thr Leu Tyr Leu Met Thr Arg Pro Lys Pro Val Tyr
162     65                  70                  75                  80
163     Leu Val Asp Phe Ser Cys Tyr Leu Pro Pro Ser His Leu Lys Ala Ser
164                 85                  90                  95
165     Thr Gln Arg Ile Met Gln His Val Arg Leu Val Arg Glu Ala Gly Ala
166                 100                 105                 110
167     Trp Lys Gln Glu Ser Asp Tyr Leu Met Asp Phe Cys Glu Lys Ile Leu
168             115                 120                 125
169     Glu Arg Ser Gly Leu Gly Gln Glu Thr Tyr Val Pro Glu Gly Leu Gln
170         130                 135                 140
171     Thr Leu Pro Leu Gln Gln Asn Leu Ala Val Ser Arg Ile Glu Thr Glu
172     145                 150                 155                 160
173     Glu Val Ile Ile Gly Ala Val Asp Asn Leu Phe Arg Asn Thr Gly Ile
174                 165                 170                 175
175     Ser Pro Ser Asp Ile Gly Ile Leu Val Val Asn Ser Ser Thr Phe Asn
176                 180                 185                 190
177     Pro Thr Pro Ser Leu Ser Ser Ile Leu Val Asn Lys Phe Lys Leu Arg
178             195                 200                 205
179     Asp Asn Ile Lys Ser Leu Asn Leu Gly Gly Met Gly Cys Ser Ala Gly
180         210                 215                 220
181     Val Ile Ala Ile Asp Ala Ala Lys Ser Leu Leu Gln Val His Arg Asn
182     225                 230                 235                 240
183     Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Asn Leu Tyr
184                 245                 250                 255
185     Met Gly Asn Asn Lys Ser Met Leu Val Thr Asn Cys Leu Phe Arg Ile
186                 260                 265                 270
187     Gly Gly Ala Ala Ile Leu Leu Ser Asn Arg Ser Ile Asp Arg Lys Arg
188             275                 280                 285
189     Ala Lys Tyr Glu Leu Val His Thr Val Arg Val His Thr Gly Ala Asp
190         290                 295                 300
191     Asp Arg Ser Tyr Glu Cys Ala Thr Gln Glu Glu Asp Glu Asp Gly Ile
192     305                 310                 315                 320
193     Val Gly Val Ser Leu Ser Lys Asn Leu Pro Met Val Ala Ala Arg Thr
194                 325                 330                 335
195     Leu Lys Ile Asn Ile Ala Thr Leu Gly Pro Leu Val Leu Pro Ile Ser
196                 340                 345                 350
197     Glu Lys Phe His Phe Phe Val Arg Phe Val Lys Lys Lys Phe Leu Asn
198             355                 360                 365
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199        Pro Lys Leu Lys His Tyr Ile Pro Asp Phe Lys Leu Ala Phe Glu His
200            370                 375                 380
201        Phe Cys Ile His Ala Gly Gly Arg Ala Leu Ile Asp Glu Met Glu Lys
202        385                 390                 395                 400
203        Asn Leu His Leu Thr Pro Leu Asp Val Glu Ala Ser Arg Met Thr Leu
204                        405                 410                 415
205        His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu Leu Ala
206                    420                 425                 430
207        Tyr Thr Glu Ala Lys Gly Arg Met Thr Lys Gly Asp Arg Ile Trp Gln
208            435                 440                 445
209        Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ser Val Trp Val Ala
210            450                 455                 460
211        Leu Arg Asn Val Lys Pro Ser Thr Asn Asn Pro Trp Glu Gln Cys Leu
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223        gcaggattag ccatgaaagg atctaagatc aacgtagaag atctccaaaa gttctccctc     180
224        caccatacac agaacaacct ccaaaccata agccttctat tgtttcttgt cgtttttgtg     240
225        tggatcctct acatgttaac ccgacctaaa cccgtttacc ttgttgattt ctcctgctac     300
226        cttccaccgt cgcatctcaa ggtcagtatc caaaccctaa tgggacacgc aagacgtgca     360
227        agagaagcag gcatgtgttg gaagaacaaa gagagcgacc atttagttga cttccaggag     420
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229        ttcccacttc agcaaggcat gggtgcttca cgtaaagaga cggaagaagt aatcttcgga     540
230        gctcttgaca atcttttcg caacaccggt gtaaaacctg atgatatcgg tatattggtg      600
231        gtgaattcta gcacgtttaa tccaactcca tcactcgcct ccatgattgt gaacaagtac     660
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233        atagctgttg atgtcgctaa gggattacta caagttcata ggaacactta tgctattgta     780
234        gtaagcacag agaacatcac tcagaactta tacttgggga aaaacaaatc aatgctagtc     840
235        acaaactgtt tgttccgcgt tggtggtgct gcggttctgc tttcaaacag atctagagac     900
236        cgtaaccgcg ccaaatacga gcttgttcac accgtacgga tccataccgg atcagatgat     960
237        aggtcgttcg aatgtgcgac acaagaagag gatgaagatg gtataattgg agttaccttg    1020
238        acaaagaatc tacctatggt ggctgcaagg actcttaaga taaatatcgc aactttgggt    1080
239        cctcttgtac ttccattaaa agagaagcta gccttcttta ttacttttgt caagaagaag    1140
240        tatttcaagc cagagttaag gaattataca ccagatttca agcttgcctt tgagcatttc    1200
241        tgtatccacg ctggtggaag agctctaata gatgagctgg agaagaacct taagctttct    1260
242        ccgttacacg tagaggcgtc aagaatgaca ctacacaggt ttggtaacac ttcttctagc    1320
243        tcaatctggt acgagttagc ttatacagaa gctaaaggaa ggatgaagga aggagatagg    1380
244        atttggcaga ttgctttggg gtcaggtttt aagtgtaaca gttcagtatg ggtggctctg    1440
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248 <210> SEQ ID NO: 6
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VERIFICATION SUMMARY
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